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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,125

DATE: 05/14/2002

TIME: 15:02:47

Input Set : N:\Crif3\RULE60\10067125.txt

Output Set: N:\CRF3\05142002\J067125.raw

3 <110> APPLICANT: Baker, Brenda F.
4 Cowsert, Lex M.
5 Monia, Brett P.
6 Xu, Xiaoxing S.
8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
10 <130> FILE REFERENCE: ISPH-0321
12 <140> CURRENT APPLICATION NUMBER: 10/067,125
13 <141> CURRENT FILING DATE: 2002-02-04
15 <150> PRIOR APPLICATION NUMBER: 09/167,109
16 <151> PRIOR FILING DATE: 1998-10-06
18 <160> NUMBER OF SEQ ID NOS: 228
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21 <211> LENGTH: 2380
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (76)..(1326)
29 <300> PUBLICATION INFORMATION:
30 <308> DATABASE ACCESSION NO: U19261 Genbank
31 <309> DATABASE ENTRY DATE: 1995-02-21
33 <400> SEQUENCE: 1
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37 gcctggaacc ctgag atg gcc tcc agc tca ggc agc agt cct cgc ccg gcc 111
38 Met Ala Ser Ser Ser Gly Ser Ser Pro Arg Pro Ala
39 1 5 10
41 cct gat gag aat gag ttt ccc ttt ggg tgc cct ccc acc gtc tgc cag 159
42 Pro Asp Glu Asn Glu Phe Pro Phe Gly Cys Pro Pro Thr Val Cys Gln
43 15 20 25
45 gac cca aag gag ccc agg gct ctc tgc tgt gca ggc tgt ctc tct gag 207
46 Asp Pro Lys Glu Pro Arg Ala Leu Cys Cys Ala Gly Cys Leu Ser Glu
47 30 35 40
49 aac ccg agg aat ggc gag gat cag atc tgc ccc aaa tgc aga ggg gaa 255
50 Asn Pro Arg Asn Gly Glu Asp Gln Ile Cys Pro Lys Cys Arg Gly Glu
51 45 50 55 60
53 gac ctc cag tct ata agc cca gga agc cgt ctt cga act cag gag aag 303
54 Asp Leu Gln Ser Ile Ser Pro Gly Ser Arg Leu Arg Thr Gln Glu Lys
55 65 70 75
57 gct cac ccc gag gtg gct gag gct gga att ggg tgc ccc ttt gca ggt 351
58 Ala His Pro Glu Val Ala Glu Ala Gly Ile Gly Cys Pro Phe Ala Gly
59 80 85 90
61 gtc ggc tgc tcc ttc aag gga agc cca cag tct gtg caa gag cat gag 399
62 Val Gly Cys Ser Phe Lys Gly Ser Pro Gln Ser Val Gln Glu His Glu

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63          95          100          105
65 gtc acc tcc cag acc tcc cac cta aac ctg ctg ttg ggg ttc atg aaa 447
66 Val Thr Ser Gln Thr Ser His Leu Asn Leu Leu Gly Phe Met Lys
67          110          115          120
69 cag tgg aag gcc cgg ctg ggc tgt ggc ctg gag tct ggg ccc atg gcc 495
70 Gln Trp Lys Ala Arg Leu Gly Cys Gly Leu Glu Ser Gly Pro Met Ala
71 125          130          135          140
73 ctg gag cag aac ctg tca gac ctg cag ctg cag gca gcc gtg gaa gtg 543
74 Leu Glu Gln Asn Leu Ser Asp Leu Gln Leu Gln Ala Ala Val Glu Val
75          145          150          155
77 gcg ggg gac ctg gag gtc gat tgc tac cgg gca ccc tgc tcc gag agc 591
78 Ala Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Ser Glu Ser
79          160          165          170
81 cag gag gag ctg gcc ctg cag cac ttc atg aag gag aag ctt ctg gct 639
82 Gln Glu Glu Leu Ala Leu Gln His Phe Met Lys Glu Lys Leu Leu Ala
83          175          180          185
85 gag ctg gag ggg aag ctg cgt gtg ttt gag aac att gtt gct gtc ctc 687
86 Glu Leu Glu Gly Lys Leu Arg Val Phe Glu Asn Ile Val Ala Val Leu
87          190          195          200
89 aac aag gag gtg gag gcc tcc cac ctg gcc ctg gcc acc tct atc cac 735
90 Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Thr Ser Ile His
91 205          210          215          220
93 cag agc cag ctg gac cgt gag cgc atc ctg agc ttg gag cag agg gtg 783
94 Gln Ser Gln Leu Asp Arg Glu Arg Ile Leu Ser Leu Glu Gln Arg Val
95          225          230          235
97 gtg gag ctt cag cag acc ctg gcc cag aaa gac cag gcc ctg ggc aag 831
98 Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp Gln Ala Leu Gly Lys
99          240          245          250
101 ctg gag cag agc ttg cgc ctc atg gag gag gcc tcc ttc gat ggc act 879
102 Leu Glu Gln Ser Leu Arg Leu Met Glu Glu Ala Ser Phe Asp Gly Thr
103          255          260          265
105 ttc ctg tgg aag atc acc aat gtc acc agg cgg tgc cat gag tcg gcc 927
106 Phe Leu Trp Lys Ile Thr Asn Val Thr Arg Arg Cys His Glu Ser Ala
107          270          275          280
109 tgt ggc agg acc gtc agc ctc ttc tcc cca gcc ttc tac act gcc aag 975
110 Cys Gly Arg Thr Val Ser Leu Phe Ser Pro Ala Phe Tyr Thr Ala Lys
111 285          290          295          300
113 tat ggc tac aag ttg tgc ctg cgg ctg tac ctg aat gga gat ggc act 1023
114 Tyr Gly Tyr Lys Leu Cys Leu Arg Leu Tyr Leu Asn Gly Asp Gly Thr
115          305          310          315
117 gga aag aga acc cat ctg tcg ctc ttc atc gtg atc atg aga ggg gag 1071
118 Gly Lys Arg Thr His Leu Ser Leu Phe Ile Val Ile Met Arg Gly Glu
119          320          325          330
121 tat gat gcg ctg ctg ccg tgg ccc ttc cgg aac aag gtc acc ttc atg 1119
122 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met
123          335          340          345
125 ctg ctg gac cag aac aac cgt gag cac gcc att gac gcc ttc cgg cct 1167
126 Leu Leu Asp Gln Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro
127          350          355          360

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129 gac cta agc tca gcg tcc ttc cag agg ccc cag agt gaa acc aac gtg 1215
130 Asp Leu Ser Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val
131 365 370 375 380
133 gcc agt gga tgc cca ctc ttc ttc ccc ctc agc aaa ctg cag tca ccc 1263
134 Ala Ser Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro
135 385 390 395
137 aag cac gcc tac gtg aag gac gac aca atg ttc ctc aag tgc att gtg 1311
138 Lys His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val
139 400 405 410
141 gag acc agc act tag ggtgggagg gctcctgagg gagctccaac tcagaaggga 1366
142 Glu Thr Ser Thr
143 415
145 gctagccaga ggactgtgat gccctgccct tggcacccaa gacctcaggg cacaagatg 1426
147 ggtgaaggct ggcgatgcc aagcaagact gaggggtcga cttcgggctg gccatctggt 1486
149 taggatggca ggacgtgggc tgggcccaca aaggcaaagg gtccagaagg agacaggcag 1546
151 agctgctccc ctctgcacgg accatgcgac actgggaggc cagtgcagca ctccggcccc 1606
153 gaatgttgag gtggactctc accaaatgag aagaaaatgg aaccaggctt ggaaccgtag 1666
155 gacccaagca gagaagctct cgggctagga agatctctgc agggccgcca gggagacctg 1726
157 gacacaggcc tgctctcttt ttctccaggg tcagaaacag gaccgggtgg aagggatggg 1786
159 gtgccagttt gaatgcagtc tgtccaggct cgtcattgga ggtgaacaag caaaccagga 1846
161 cggctccact aggacttcaa attgggggtt ggatttgaag acttttaagt ttcttccag 1906
163 cccagaaagt ctctcattct agcctcctgg cccagggtgag tcctagagct acaggggttc 1966
165 tggaaacatt caggagcttc ctgtcctccc agctcctcac tcaccttcag taacccccac 2026
167 tggactgacc tgggccacag ggcacctgcc accctgggcc tggcagctca gcttcccaac 2086
169 acgcaggagc acaccagcc cccacatcct gtgcctccat cagctaaaca ccacgtcact 2146
171 tcatgcaggc gaaaccagc cactgtgagc tcccagggtg agccagaggc acctcaagaa 2206
173 gaagaggggc ataaactttc ctcttctctg ctagaggccc cacttttggg gctttccaga 2266
175 atcccgtaac acctgattaa ctgaggcatc cacttctttc agcagactga tcaggacctc 2326
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179 <210> SEQ ID NO: 2
180 <211> LENGTH: 2262
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <220> FEATURE:
185 <221> NAME/KEY: CDS
186 <222> LOCATION: (55)..(1560)
188 <300> PUBLICATION INFORMATION:
189 <308> DATABASE ACCESSION NO: U12597 Genbank
190 <309> DATABASE ENTRY DATE: 1996-02-16
192 <400> SEQUENCE: 2
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195 Met
196 1
198 gct gca gct agc gtg acc ccc cct ggc tcc ctg gag ttg cta cag ccc 105
199 Ala Ala Ala Ser Val Thr Pro Pro Gly Ser Leu Glu Leu Leu Gln Pro
200 5 10 15
202 ggc ttc tcc aag acc ctc ctg ggg acc aag ctg gaa gcc aag tac ctg 153
203 Gly Phe Ser Lys Thr Leu Leu Gly Thr Lys Leu Glu Ala Lys Tyr Leu
204 20 25 30

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Input Set : N:\Crf3\RULE60\10067125.txt

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206 tgc tcc gcc tgc aga aac gtc ctc cgc agg ccc ttc cag gcg cag tgt 201
207 Cys Ser Ala Cys Arg Asn Val Leu Arg Arg Pro Phe Gln Ala Gln Cys
208      35      40      45
210 ggc cac cgg tac tgc tcc ttc tgc ctg gcc agc atc ctc agc tct ggg 249
211 Gly His Arg Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Ser Ser Gly
212 50      55      60      65
214 cct cag aac tgt gct gcc tgt gtt cac gag ggc ata tat gaa gaa ggc 297
215 Pro Gln Asn Cys Ala Ala Cys Val His Glu Gly Ile Tyr Glu Glu Gly
216      70      75      80
218 att tct att tta gaa agc agt tcg gcc ttc cca gat aat gct gcc cgc 345
219 Ile Ser Ile Leu Glu Ser Ser Ser Ala Phe Pro Asp Asn Ala Ala Arg
220      85      90      95
222 agg gag gtg gag agc ctg ccg gcc gtc tgt ccc agt gat gga tgc acc 393
223 Arg Glu Val Glu Ser Leu Pro Ala Val Cys Pro Ser Asp Gly Cys Thr
224      100      105      110
226 tgg aag ggg acc ctg aaa gaa tac gag agc tgc cac gaa ggc cgc tgc 441
227 Trp Lys Gly Thr Leu Lys Glu Tyr Glu Ser Cys His Glu Gly Arg Cys
228      115      120      125
230 ccg ctc atg ctg acc gaa tgt ccc gcg tgt aaa ggc ctg gtc cgc ctt 489
231 Pro Leu Met Leu Thr Glu Cys Pro Ala Cys Lys Gly Leu Val Arg Leu
232 130      135      140      145
234 ggt gaa aag gag cgc cac ctg gag cac gag tgc ccg gag aga agc ctg 537
235 Gly Glu Lys Glu Arg His Leu Glu His Glu Cys Pro Glu Arg Ser Leu
236      150      155      160
238 agc tgc cgg cat tgc cgg gca ccc tgc tgc gga gca gac gtg aag gcg 585
239 Ser Cys Arg His Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys Ala
240      165      170      175
242 cac cac gag gtc tgc ccc aag ttc ccc tta act tgt gac ggc tgc ggc 633
243 His His Glu Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly
244      180      185      190
246 aag aag aag atc ccc cgg gag aag ttt cag gac cac gtc aag act tgt 681
247 Lys Lys Lys Ile Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr Cys
248      195      200      205
250 ggc aag tgt cga gtc cct tgc aga ttc cac gcc atc ggc tgc ctc gag 729
251 Gly Lys Cys Arg Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu Glu
252 210      215      220      225
254 acg gta gag ggt gag aaa cag cag gag cac gag gtg cag tgg ctg cgg 777
255 Thr Val Glu Gly Glu Lys Gln Gln Glu His Glu Val Gln Trp Leu Arg
256      230      235      240
258 gag cac ctg gcc atg cta ctg agc tcg gtg ctg gag gca aag ccc ctc 825
259 Glu His Leu Ala Met Leu Leu Ser Ser Val Leu Glu Ala Lys Pro Leu
260      245      250      255
262 ttg gga gac cag agc cac gcg ggg tca gag ctc ctg cag agg tgc gag 873
263 Leu Gly Asp Gln Ser His Ala Gly Ser Glu Leu Leu Gln Arg Cys Glu
264      260      265      270
266 agc ctg gag aag aag acg gcc act ttt gag aac att gtc tgc gtc ctg 921
267 Ser Leu Glu Lys Lys Thr Ala Thr Phe Glu Asn Ile Val Cys Val Leu
268      275      280      285
270 aac cgg gag gtg gag agg gtg gcc atg act gcc gag gcc tgc agc cgg 969

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Input Set : N:\Crif3\RULE60\10067125.txt

Output Set: N:\CRF3\05142002\J067125.raw

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271 Asn Arg Glu Val Glu Arg Val Ala Met Thr Ala Glu Ala Cys Ser Arg
272 290                295                300                305
274 cag cac cgg ctg gac caa gac aag att gaa gcc ctg agt agc aag gtg 1017
275 Gln His Arg Leu Asp Gln Asp Lys Ile Glu Ala Leu Ser Ser Lys Val
276                310                315                320
278 cag cag ctg gag agg agc att ggc ctc aag gac ctg gcg atg gct gac 1065
279 Gln Gln Leu Glu Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala Asp
280                325                330                335
282 ttg gag cag aag gtc agg ccc ttc cag gcg cag tgt ggc cac cgg tac 1113
283 Leu Glu Gln Lys Val Arg Pro Phe Gln Ala Gln Cys Gly His Arg Tyr
284                340                345                350
286 tgc tcc ttc tgc ctg gcc agc atc ctc agg aag ctc cag gaa gct gtg 1161
287 Cys Ser Phe Cys Leu Ala Ser Ile Leu Arg Lys Leu Gln Glu Ala Val
288                355                360                365
290 gct ggc cgc ata ccc gcc atc ttc tcc cca gcc ttc tac acc agc agg 1209
291 Ala Gly Arg Ile Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg
292 370                375                380                385
294 tac ggc tac aag atg tgt ctg cgt atc tac ctg aac ggc gac ggc acc 1257
295 Tyr Gly Tyr Lys Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp Gly Thr
296                390                395                400
298 ggg cga gga aca cac ctg tcc ctc ttc ttt gtg gtg atg aag ggc ccg 1305
299 Gly Arg Gly Thr His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro
300                405                410                415
302 aat gac gcc ctg ctg cgg tgg ccc ttc aac cag aag gtg acc tta atg 1353
303 Asn Asp Ala Leu Leu Arg Trp Pro Phe Asn Gln Lys Val Thr Leu Met
304                420                425                430
306 ctg ctc gac cag aat aac cgg gag cac gtg att gac gcc ttc agg ccc 1401
307 Leu Leu Asp Gln Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro
308                435                440                445
310 gac gtg act tca tcc tct ttt cag agg cca gtc aac gac atg aac atc 1449
311 Asp Val Thr Ser Ser Ser Phe Gln Arg Pro Val Asn Asp Met Asn Ile
312 450                455                460                465
314 gca agc ggc tgc ccc ctc ttc tgc ccc gtc tcc aag atg gag gca aag 1497
315 Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala Lys
316                470                475                480
318 aat tcc tac gtg cgg gac gat gcc atc ttc atc aag gcc att gtg gac 1545
319 Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile Val Asp
320                485                490                495
322 ctg aca ggg ctc taa ctgcccccta ctgggtgtctg ggggttgggg gcagccaggc 1600
323 Leu Thr Gly Leu
324                500
326 acagccggct cacggagggg ccaccacgct gggccagggt ctcaactgtac aagtgggcag 1660
328 gggccccgct tgggcgcttg ggaggggtgc ggcctgcagc caagttcact gtcacggggg 1720
330 aaggagccac cagccagtcc tcagatttca gagactgcgg aggggcttgg cagacggctc 1780
332 tagccaaggg ctgtggtggc attggccgag ggtcttcggg tgcttccag cacaagctgc 1840
334 ccttgctgtc ctgtgcagtg aaggagagag ccctgggtgg gggacactca gagtgggagc 1900
336 acatcccagc agtgcccatg tagcaggagc acagtggatg gccttgtgtc cctcgggcat 1960
338 gacaggcaga aacgagggct gctccaggag aagggcctcc tgctggccag agcaaggaag 2020
340 gctgagcagc ttggttctcc cctctggccc ctggagagaa gggagcattc ctgaccctc 2080

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,125

DATE: 05/14/2002

TIME: 15:02:48

Input Set : N:\Crf3\RULE60\10067125.txt

Output Set: N:\CRF3\05142002\J067125.raw

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L:2060 M:283 W: Missing Blank Line separator, <220> field identifier
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L:3159 M:283 W: Missing Blank Line separator, <220> field identifier